4 12:39:38 2002

Fri Jan

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

January 3, 2002, 21:32:44; Search time 38.81 Seconds (without alignments) 1761.650 Million cell updates/sec Run on:

US-09-497-822h-19 Perfect score:

4912 1 MEVQLGLGRVYPRPPSKTYR....SVQVPKILSGKVKPIYFHTQ Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 522463 seqs, 74073290 residues Searched:

522463

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
AfstAng Xirst 45 summaries

A_Geneseq_1101

/SIDS2/gcgdata/geneseq/genesegp/Aa1984 DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:*

	Description		muruyen receptor.	Hullan androgen rec	nument androgen rec	Human androgen rec	numan androgen rec	Human androgen rec	Rat androgen recep	rat androgen recep	ran androgen recep	Ligand binding dom	TrpE/androgen rece
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ALIGNMENTS

AAW14783 RESULT

AAW14783 standard; Protein; 919 AA.

AAW14783;

(first entry) 22-JUN-1997

Androgen receptor.

Androgen receptor; acidic fibroblast growth factor; aFGF; antisense; benign prostatic hyperplasia; prostate cancer; therapy.

Homo sapiens

WO9711170-A1 27-MAR-1997 X Z X Q

96WO-US15081. 20-SEP-1996; (WORC-) WORCESTER FOUND BIOMEDICAL RES

95US-0004018

20-SEP-1995;

Samecnik PA

WPI; 1997-202879/18. N-PSDB; AAT63407.

Oligonucleotide(s) antisense to human androgen receptor and acidic FGF genes - used to inhibit gene expression, for the treatment of benign prostatic hyperplasia

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               Human androgen receptor (AAW14783) binds testosterone and, acting at the transcriptional level, regulates the growth of normal prostatic cells. Antisense oligonucleotides (see also AAT63200, AAT63404-05) based on an androgen receptor cDNA clone (see also AAT63407) can be used to prevent androgen receptor gene expression, thereby inhibiting the growth or survival of prostatic cells for the treatment of benign prostatic hyperplasia and prostate cancer.
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Disclosure; Page 22-28; 51pp; English.
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This.sequence represents the human androgen receptor (AR) amino acid sequence. The invention relates to a fragment of the AR corresponding to amino acids 234-391 (see ARY18913). The fragment mediates and androgen-independent activation of the AR. The androgen receptor acts as a transcription factor, regulating the expression of certain a transcription factor, regulating the expression of certain cardrogen-responsive genes. Interaction of the AR with the protein kinase androgen-responsive genes. Interaction of the AR with the protein kinase independent region. The AR fragment and peptides derived from it can be independent receptor, as activation domains, and as a tool for screening candrogen receptor, as activation domains, and as a tool for screening con receptor, as activation domains, and as a tool for screening correctively limit androgen mediated disease progression. These diseases effectively limit androgen mediated disease progression. These diseases include cancer, benign prostatic hyperplasia, hirusutism, androgenic alopecia, acne, breast cancer, Kennedy disease, and especially prostate for the treatment of androgen-eacidisted diseases, especially prostate fumours in patients deprived of androgen.
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89WO-US01548

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Human androgen receptor; ployclonal antibody; cancer.
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Androgen receptor protein (AR) is used to produce mono- or poly-clonal antibodies. These are used for the detection and quantification of AR in the presence of endogenous androgen, as androgen will not interfere with binding. They may be used in assays to determine and quantify cellular distribution of AR in tumour tissue, and are esp. useful for evaluating prostate cancers to determine responsiveness to androgen withdrawal therapy.
                                                                                                                                      prodn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 QQQQQQQQQQQQQQQQQQQQQQETSPRQQQQQQGEDGSPQAHRRGPTGYLVLDEEQQPSQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding androgen receptor protein – useful for transforming eukaryotic hosts for protein expression and subsequent antibody 
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 919;
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                                    DB;
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Pred. No. 0;
0; Mismatches
                                 Joseph DR, Lubahn
(UYNC=) UNIVERSITY OF NORTH CAROLINA.
                                                                                                                                                             4; 41pp; English.
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Best Local Similarity 99.5
Matches 918; Conservative
                              Wilson EM,
                                                            1989-324206/44.
                                                                                                                                                                                                                                                                                                                       919 AA;
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                                                                             N-PSDB; AAN91772
                              French FS,
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AAP93109 RESULT

(first entry)

19-MAR-1990

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Human androgen receptor

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Proapoptotic; dependence domain; p75NTR; androgen receptor; DCC; huntingtin polypeptide; Machado-Joseph disease; SCA1; SCA2; SCA6; atrophin-1; cell death; apoptosis; Huntington's disease; head trauma; Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; stroke; dentatorubropallidoluysian atrophy; cell proliferation; cell survival; neoplastic; malignant; autoimmune; fibrotic.
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                                        SRNDCTIDKFRRKNCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGEASSTTSPTEETT
                                                                                 KWAKALPGFRNLHVDDQMAVIQYSWMGLMVFAMGWRSFTNVNSRMLYFAPDLVFNEYRMH
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                              MRLETARDHVLPIDYYFPPQKTCLICGDEASGCHYGALTCGSCKVFFKRAAEGKQKYLCA
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dependence polypeptides consisting of p75NTR, androgen receptor, DCC, huntingtin polypeptide, Machado-Joseph disease gene product, SCA1, SCA2, SCA6 and atrophin-1 polypeptide. The proapoptotic peptides are capable of inducing cell death and can be used to develop products to mediate or inhibit apoptosis. The methods can be used for reducing the severity of a proapoptotic dependence domain mediated pathological conditions e.g. Spinocerebellar ataxias, dentatorubropallidoluysian atrophy. Machado-Joseph disease, Stroke or head trauma. They can also be used for reducing the severity of a pathological condition mediated by upregulated cell proliferation or cell survival e.g. neoplastic, malignant, autoimmune or fibrotic conditions. This sequence represents a human androgen receptor described in the method of the invention.
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Pred. No. 6.4e-318;
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          YIKELDRIIACKRKNPTSCSRRFYQLTKLLDSVQPIARELHQFTFDLLIKSHMVSVDFPE
                                             This sequence was deduced from a cDNA clone isolated by screening commercially available human testis and prostate lambda gtll cDNA libraries. The sequence is very similar to that of rat AR and in the DNA-binding domain it is identical to that of rAR DNA-binding domain. Homology comparisons with other known steroid receptors indicate that hAR is more closely related to glucocorticoid, mineralo-corticoid and progesterone receptors than to v-erb-A or t receptors for oestrogen, vitamin D and thyroid hormones.
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Pred. No. 3.4e-317;
1; Mismatches 2;
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/label= DNA-binding domain
/note= "cysteine-rich"
                                                                                                                                                                                                            bNA-binding protein; steroid hormone.
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                                                                                                                        LCKAVSVSMGLGVEALBHLSPGEQLRGDCWYAPLLGVPPAVRPTPCAPLAECKGSLLDDS
                                PQSALECHPERGCVPEPGAAVAASKGLPQQLPAPPDEDDSAAPSTLSLLGPTFPGLSSCS
                                             ADLKDILSEASTMQLLQQQQGEAVSEGSSSGRAREASGAPTSSKDNYLGGTST1SDNAKE
                                                                                          AGAVAPYGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVPYPSPTCVKSEMGPWMDSYSGP
                                                                                                                                                                                                                                                                                                                                     aeavapygytrppqglagqesdftapdvwypggmvsrvpypsptcvksemgpwmdsysgp
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                                                                                                                                                                                                                                                                                                                                                                                                                        YIKELDRIIACKRKNPTSCSRRFYQLTKLLDSVQPIARELHQFTFDLLIKSHMVSVDFPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    718 HVVKWAKALPGFRNLHVDDQMAVIQYSWMGLMVFAMGWRSFTNVNSRMLYFAPDLVFNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RMHKSRMYSQCVRMRHLSQEFGWLQITPQEFLCMKALLLFSIIPVDGLKNQKFFDELRMN
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2; Indels

98.58;

Similarity

Best Local Sim Matches 912;

Conservative

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Androgen receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 gpgsalechpergcypepgaavaaskglpgqlpappdeddsaapstlsllgptfpglssc 172
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                                                                                                                                                                                                           polypeptide(s) - able receptor assay and
                                                                                                                                                                                                                                                               The protein is used to raise antibodies for receptor assays and for affinity purification.

The 98 kp product starts at the first Met codon; the 79 kD product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SADLKDILSEASTMOLLOQQQQEAVSEGSSSGRAREASGAPTSSKDNYLGGTSTISDNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 SAGKSTEDTAEYSPFKGGYTKGLEGESLGCSGSAAAGSSGTLELPSTLSLYKSGALDEAA
                                                                                                                                                                                                                                                                                                                                                                        1 MEVQLGLGRVYPRPPSKTYRGAFQNLFQSVREVIQNPGPRHPEAASAAPPGASLLL
                                                                                                                                                                                                                                                                                                                                                                                   Length 919;
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                                                                                                                                                                                                                                                                                                                                      Score 4814; DB 10;
Pred. No. 2.8e-316;
0; Mismatches 3;
                                                                                                                                                                                                            TR2 p
                                                                                                                                                                                                             encoding new androgen receptor and DNA, and derived antibodies, useful
                                                         polypeptide
                               kD polypeptide
     Location/Qualifiers
                                                          /product=79 kD
                    /product=98 km
185.919
/*tag= b
                                                                                                                                                                                                                                                 Claim 8; Fig 3; 60pp; English
                                                                                                                                                ARCH DEVELOPMENT CORP
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.4%
Matches 912; Conservative
                                                                                                              89WO-US01238
                                                                                                                                88US-0176107
                                                                                                                                                                                                                                                                                            starts from the second.
                                                                                                                                                                                    1989-309501/42
                                                                                                                                                                                                                                                                                                              919 AA;
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                                                                                                                                                                                                                                purification.
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                                                                                                               24-MAR-1989;
                                                                             WO8909223-A.
                                                                                             05-0CT-1989.
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                                                                                                                                                                                                                                                                                                                                                                                     encoding new androgen receptor and TR2 polypeptide(s) - able DNA, and derived antibodies, useful for receptor assay and
                                                           596
                                                                                                                   VHVVKWAKALPGFRNLHVDDQMAVIQYSWMGLMVFAMGWRSFTNVNSRMLYFAPDLVFNE
                                                                                                                                                                                                                                                            EETTQKLTVSH1EGYECQPIFLNVLEA1EPGVVCAGHDNNQPDSFAALLSSLNELGERQL
EAGAVAPYGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVPYPSPTCVKSEMGPWMDSYSG
                 PYGDMRLETARDHVLPIDYYFPPQKTCLICGDEASGCHYGALTCGSCKVFFKRAAEGKQK
                                                                          kD polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TR2)polypeptide;
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170..902
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N-PSDB; AAN91578.
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DLLIKSHMVSVDFPEMMAEIISVQVPKILSGKVKPIYFHTQ 923
                                         French FS, Wilson EM, Joseph DR, Lubahn DB;
                                                                                                                                                                                                                                                                        UNIVERSITY OF NORTH CAROLINA
                                                                                                ΑA
                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig. 5; 41pp; English.
                                                                                              902
                                                                                               protein;
                                                                                                                                                                                                                                       89WO-US01548.
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                                                                                                                                 entry)
                                                                                                                                                androgen receptor.
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                                                                                           AAP93110 standard;
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                                                                                                                               19-MAR-1990
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                                 The protein is used to raise antibodies for receptor assays and for affinity purification.
The 98 kD product starts at the first Met codon; the 79 kD product starts from the second.
                                      for receptor assays and for
                                                                                                                                                                                       1 MEVOLGLGRVYPRPPSKTYRGAFONLFOSVREVIONFGPRHPEAASAAPPGASL/LLQQO
                                                                                                                                                                                                                                                              sadikdilseagtmqllqqqqqqqqqqqqqqqqqqqqqqqqvisegsssvrareatgapss
                                                                                                                                                                                                                                                                                 SKDNYLGGTSTISDNAKELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYAPLLGVPPAVR
                                                                                                                                                                                                                                                                                                                    PTPCAPLAECKGSLLDDSAGKSTEDTAEYSPFKGGYTKGLEGESLGCSGSAAAGSSGTLE
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                                                                                                          Length 902;
                                                                                                                                                  ; Score 4201.5; DB 10; Lengt
; Pred. No. 5.6e-275;
36; Mismatches 52; Indels
                Claim 8; Fig 3; 60pp; English.
                                                                                                      Query Match
Best Local Similarity 84.6%;
Matches 796; Conservative 36
                                                                                                                                                                                                                                               SADLKDILSEASTMQLL-
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purification
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Androgen receptor protein (AR) is used to produce mono- or poly-clonal antibodies. These are used for the detection and quantification of AR in the presence of endogenous androgen, as androgen will not interfere with binding. They may be used in assays to determine and quantify cellular distribution of AR in tumour tissue, and are esp. useful for evaluating prostate cancers to determine responsiveness to androgen withdrawal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat androgen receptor; monoclonal antibody; ployclonal antibody; cancer.
861
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Pred. No. 6.5e-275;
5; Mismatches 52; Indels 57;
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                                                                                                                                                                                                        CKVFFKRAAEGKQKYLCASRNDCTIDKFRRKNCPSCRLRKCYEAGMTLGARKLKKLGNLK
                                                                                                                                                        SRMLYFAPDLVFNEYRMHKSRMYSQCVRMRHLSQEFGWLQITPQEFLCMKALLLFSIIPV
                                                                                                                                                                                                                                                  DGLKNQKFFDELRMNY1KELDRI1ACKRKNPTSCSRRFYQLTKLLDSVQPIARELHQFTF
       PTPCAPLAECKGSLLDDSAGKSTEDTAEYSPFKGGYTKGLEGESLGCSGSAAAGSSGTLE
                                                                          AAAAQCRYGDLASLHGAGAAGPGSGSPSAAASSSWHTLFTAEEGQLYGPCGGGGGGGGG
                                                                                VKSEMGPWMDSYSGPYGDMRLETARDHVLPIDYYFPPQKTCLICGDEASGCHYGALTCGS
 SKDNYLGGTSTISDNAKELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYAPILGVPPAVR
                                                                                                 GCGGGGGGGGGGGGAAAPYGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVPYPSPTC
                                                                                                                                                                                                                                                                                  DLLIKSHMVSVDFPEMMAEIISVQVPKILSGKVKPIYFHTQ 923
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
540..610
/label= DNA-binding domain
/note= "cysteine-rich"
                                                                                                                                                                                                                                                                                                                                                                     protein; steroid hormone.
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                                                                                                                                                                                                                                                                                                                                                          androgen receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTPCAPLAECKGSLLDDSAGKSTEDTAEYSPFKGGYTKGLEGESLGCSGSAAAGSSGTLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            523 VKSEMGPWMDSYSGPYGDMRLETARDHVLPIDYYFPPQKTCLICGDEASGCHYGALTCGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGGGGGGGGGGAVAPYGYTRPPQGLAGQESDFTAPDVWYPGGWVSRVPYPSPTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---gggggssspsdagpvapygytrppqglasqegdfsasevwypggvvnrvpypspsc
                                                                                                                                                                                                                                  This sequence was deduced from a cDNA clone isolated by screening a rat ventral prostate lambda gtll library in E.coli Y1090. The sequence is very similar to that of human AR and in the DNA-binding domain it is identical to that of hAR DNA-binding domain it is identical to that of hAR DNA-binding domain it is identical to that of hAR DNA-binding mindicate that TAR is more closely related to glucocorticoid, mineralo-corticoid and progesterone receptors than to v-erb'A or treceptors for oestrogen, vitamin D and thyroid hormones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEVQLGLGRVYPRPPSKTYRGAFQNLFQSVREVIQNPGPRHPEAASAAPPGASILLLLQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 902,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57;
                                                                                                                                                   Androgen receptor and TR2 DNA binding proteins – DNA sequences and antibodies for detection and quantification methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              85.3%; Score 4187.5; DB 12
84.4%; Pred. No. 4.9e-274;
iive 37; Mismatches 53;
                                                                                                                                                                                                        Claim 25; Fig 3; 79pp; English.
89US-0438775
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 85.33
Best Local Similarity 84.43
Matches 794; Conservative
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                                    (ARCH-) ARCH. DEV
                                                                     Chang C
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17-NOV-1989;
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us-09-497-822a-19.rag

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The invention relates to a method for modulating activity of a thyroid which fits spatially and preferentially into a thyroid hormone ligand binding domain. The aromatic compound (of a specified hormone ligand binding domain. The aromatic compound (of a specified formula) can be used to increase alpha-gleerophosphate dehydrogenase (GPDH) levels, at levels which do not significantly modify cardiac GPDH levels and are indicated in the treatment of obesity. The compound also lower total plasma cholesterol and triglyceride levels and can be used as anti-dhypertiglyceridaemic agents. The compound may also be used for treating atherosclerosis and may be indicated in thyroid hormone replacement therapy in patients with compromised cardiac function. Sequences AMY21621-636 amino acid sequences of ligand binding domains of several members of the nuclear receptor superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thyroid hormone receptor; aromatic compound; ligand binding domain; alpha-glcerophosphate dehydrogenase; cardiac; obesity; triglyceride; plasma cholesterol; anti-hypertriglyceridaemic; atherosclerosis; GPDH; thyroid hormone replacement therapy; nuclear receptor.
                                     702
                                                                                             762
                                                                                                                                             SRMLYFAPDLVFNEYRMHKSRMYSQCVRMRHLSQEFGWLQITPQEFLCMKALLLFSIIPV 822
                                                                                                                                                                                                           882
562 ckvffkraaegkqkylcasrndctidkfrrkncpscrlrkcyeagmtlgarklkklgnlk 621
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                                                                                                                                                            DGLKNQKFFDELRMNYIKELDRIIACKRKNPTSCSRRFYQLTKLLDSVQPIARELHQFTF
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                                                                                                                                                                                                                                                                          Kushner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating activity of a thyroid hormone receptor
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Wagner RL, West
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                                                                                     1 gggggeagavapygytrppqglagqesdftapdvwypggmvsrvpypsptcvksemgpwm 60
                                                                                                          532 DSYSGPYGDMRLETARDHVLPIDYYFPPQKTCLJCGDEASQCHYGALTCGSCKVFFKRAA
                                                                                                                                                EGKOKYLCASRNDCTIDKFRRNCPSCRLRRCYEAGMTLGARKLKKLGNLKLQEEGEASS
                                                                                                                                                                                                 TTSPTEETTQKLTVSHIEGYECQPIFLNVLEAIEPGVVCAGHDNNQPDSFAALLSSLNEL
                                                                                                                                                                                                                                                                        LVFNEYRMHKSRMYSQCVRMRHLSQEFGWLQITPQEFLCMKALLLFSIIPVDGLKNQKFF
                                                                                                                                                                                                                                                                                                             DELRMNYIKELDRIIACKRKNPTSCSRRFYQLTKLLDSVQPIARELHQFTFDLLIKSHMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            incl. AR DNA-binding domain
                                                   ;
0
                                Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     androgen receptor; AR; DNA-binding protein; steroid hormone.
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TrpE/Androgen receptor DNA-binding domain fusion protein.
                               Score 2429; DB 20;
Pred. No. 7.9e-156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324..334
/label= 11 amino acid linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= 17 amino acid linker
                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                               SVDFPEMMAEIISVQVPKILSGKVKPIYFHTQ 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= 33kD trpE protein
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/label= 2
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                                        Similarity
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452
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                                                Matches 451;
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Sequence
                             Query Match
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Rat; androgen receptor; AR: ligand binding domain; LBD: osteopathic; crystallographic structure; AR-LBD; AR modulator; prostate cancer; age related disease; osteoporosis; muscle wasting; libido; vasotropic; protein coordinate data.
                                                                                                                                                                                                                                                                                                                                                  LRKCYEAGMTLGARKLKKLGNLKLQEEGEASSTTSPTEETTQKLTVSHIEGYECQPIFLN 679
                                                                                                                                                                                                                                                                                                                                                                                                                                  680 VLEAIEPGVVCAGHDNNQPDSFAALLSSLNELGERQLVHVVKWAKALPGFRNLHVDDQMA 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                740 VIQYSWMGLMVFAMGWRSFINVNSRMLYFAPDLVFNEYRMHKSRMYSQCVRMRHLSQEFG 799
                                                                                                                                                                                                                                                                                         515 VPYPSPTCV----KSEMGPWM----DS----YSGPYGDMRLE-TARDHVLPIDYYFPP 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          To express an androgen receptor fusion protein in E.coli, the pATH expression system was used. The trpE is insoluble so partially purified induced fusion protein is obtained by simply lysing the E.coli and precipitating the insoluble fusion protein. The fusion protein was used for immunisation to obtain monoclonal anti-AR
                                                                                                                                                                                                                                                                                                                                                                                                                                              560 QKTCLICGDEASGCHYGALTCGSCKVFFKRAAEGKQKYLCASRNDCTIDKFRRKNCPSCR
                                                                                                                                                                                                                                                                  24;
                                                               29.7%; Score 1459; DB 12; Length 630; 79.9%; Pred. No. 3.1e-90; ive 17; Mismatches 31; Indels 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat androgen receptor ligand binding domain.
                                                                                                                                                                                                                                                                     17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB97073 standard; Protein; 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000WO-US28495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                     286; Conservative
                                                                                                    Example 13; Fig 10; 79pp;
                               WPI; 1991-178048/24
N-PSDB; AAQ12008.
                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                            630 AA
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Best Local S:
Matches 286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB97073;
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New crystallographic structure of the Androgen receptor ligand binding domain, useful for identifying modulators of androgen receptors
                                                                                                                                                                                      The present sequence is the rat androgen receptor (AR) ligand-binding domain (LBD). It is provided in an example illustrating an invention relating to a new crystallographic structure of the AR-LBD. The structure comprises either an AR-LBD and an AR-LBD ligand, or an AR-LBD builthout an AR-LBD ligand (where the crystal diffracts to at least 3 angstrom resolution and has a crystal stability within 5 % of its unit cell dimensions). The AR-LBD is useful for identifying modulators of the androgen receptor, which may be used for treating prostate cancer and age related diseases such as osteoporosis, muscle wasting and loss of libido.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIACKRKNPTSCSRRFYQLTKLLDSVQPIARELHQFTFDLLIKSHMVSVDFPEMMAEIIS 904
                                                                                                                                                                                                                                                                                                                                                                                                                                              666 SH-IEGYECQPIFLNVLEAIEPGVVCAGHDNNQPDSFAALLSSLNELGERQLVHVVKWAK 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 shmiegyecqpiflnvleaiepgvvcaghdnnqpdsfaallsslnelgerqlvhvvkwak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          785 YSQCVRMRHLSQEFGWLQITPQEFLCMKALLLFSIIPVDGLKNQKFFDELRMNYIKELDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               725 ALPGFRNLHVDDQMAVIQYSWMGLMVFAMGWRSFTNVNSRMLYFAPDLVFNEYRMHKSRM
                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    androgen receptor; AR; DNA-binding protein; steroid hormone.
                                                     Salvati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TrpE/androgen receptor N-terminal domain fusion protein.
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0
                                                     Sack JS,
                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 2.5e-83;
0; Mismatches 0
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/label= 6 amino acid linker
330..571
                                                                                                                                                                                                                                                                                                                                                                                         27.5%; Score 1349.5;
99.6%; Pred. No. 2.5e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..323
/label= 33kD trpE protein
                                                     Krystek SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 AA
                                                                                                                                                                  Example; Page 27; 83pp; English.
                          BRISTOL-MYERS SQUIBB CO.
                                                                   Attar RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         905 VQVPKILSGKVKPIYFHTQ 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR12229 standard; Protein;
 99US-0159394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 27.5
Best Local Similarity 99.6
Matches 258; Conservative
                                                      Einspahr HM,
                                                                      Wang C,
                                                                                              WPI; 2001-300222/31.
                                                                                                                                                                                                                                                                                                                                                    260 AA;
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                                                                   JS,
14-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                       Sequence
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Protein
                                                         einmann
                                                                      pkarsk
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Gaps

RESULT 14

AAY21621

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17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                  To express an androgen receptor fusion protein in E.coli, the pATH expression system was used. The trpE is insoluble so partially purified induced fusion protein is obtained by simply lysing the E.coli and precipitating the insoluble fusion protein. The fusion protein was used for immunisation to obtain monoclonal anti-AR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 ·LLDDS----AGKSTEDTAEYSPFKGGYTKGLEGESLGCSGSAAAGSSGTLELPSTLSLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 ffmqdndftlfgaspesslkyd----atsrqie-----iprnsssgtlelpstlsly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEGSSSGRAREASGAPTSSKDNYLGGTSTISDNAKELCKAVSVSMGLGVEALEHLSPGEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDLASLHGAGAAGPGSGSPSAAASSSWHTLFTAEEGQLYGPC---GGGGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGGGGGEAGAVAPYGYTRPPQGLAGQESDFTAPDVWYPGGMYSRVPYPSPTCVKSEM
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                                                                                                                                                                                                                                     Androgen receptor and TR2 DNA binding proteins – DNA sequences and antibodies for detection and quantification methods
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPWMDSYSGPYGDMRLETARDHVLPIDYYFPPQKTCLICGDEASGCHYGA 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92;
                                                                                                                                                                                                                                                                                                                                                                                                                                27.2%; Score 1337.5; DB 55.5%; Pred. No. 4.4e-82; ive 39; Mismatches 92
/label= N-terminal region of
         572..576
/label= 5 amino acid linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAAPSTLSLLGPTFPGLSSCS----ADLKDILSE--
                                                                                                                                                                                                                                                                             Example 13; Fig 9; 79pp; English.
                                                                                                                        89US-0438775.
                                                                                                  90WO-US06015.
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                                                                                                                                                   ARCH DEV CORP
                                                                                                                                                                                                1991-178048/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 294; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            576 AA;
                                                                                                                                                                         Chang C;
                                                                                                                                                                                                                N-PSDB; AAQ12007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 LRGDCMYA-
                                                                                                                         17-NOV-1989;
                                                                       30-MAY-1991.
                                                                                            19-OCT-1990;
                                              WO9107423-A
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                           Liao S,
          Region
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Matches
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hormone receptor that comprises administration of an aromatic compound which fits spatially and preferentially into a thyroid hormone ligand which fits spatially and preferentially into a thyroid hormone ligand binding domain. The aromatic compound (of a specified formula) can be used to increase alpha-gloerophosphate dehydrogenase (GDBH) levels, at levels which do not significantly modify cardiac GDBH levels and are indicated in the treatment of obesity. The compound also lower total hypertriglyceridemic agents. The compound may also lower total hypertriglyceridemic agents. The compound may also be used as anti-hypertriglyceridemic agents. The compound may also be used for treating atherosclerosis and may be indicated in thyroid hormone replacement therapy in patients with compromised cardiac function. Sequences

AAY21621 = 636 amino acid sequences of ligand binding domains of several
                                                                                                                                                  Thyroid hormone receptor; aromatic compound; ligand binding domain; alpha-glcerophosphate dehydrogenase; cardiac; obesity; triglyceride; plasma cholesterol; anti-hypertriglyceridaemic; atherosclerosis; GPDH; thyroid hormone replacement therapy; nuclear receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to a method for modulating activity of a thyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 QQQQQQQQQQQQQQQQETSPRQQQQQGEDGSPQAHRRGPTGYL--VLDEEQQPSQPQSA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 dpsdektqdqqslsdvegaysraeatrgaggssssppekdsglldsvldtllapsgpgqs 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 LECHPERGCVPEPGAAVAASKG--LPQQLPAPPDEDDSAAPSTLSLLGPTFP-----GL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSCSADLKDILSE--ASTMQLL--------00000EAVS-EGSSSGRAREASG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----qpsppacevtsswclfgpelp----edppaapatgrvlsplmsrsgckvgd 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kushner PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating activity of a thyroid hormone receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1261; DB 20;
Pred. No. 1.2e-76;
8; Mismatches 318;
                                                                                                                Ligand binding domain of nuclear receptor hPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         members of the nuclear receptor superfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ), Fletterick RJ,
Wagner RL, West F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 3A-R; 447pp; English
      AA.
AAY21621 standard; protein; 933
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                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
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Scanlan TS, Shiau AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-357810/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JW,
                                                                            11-AUG-1999
                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                       W09926966-A2
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                                        AAY21621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGLMVFAMGWRSFTNVNSRMLYFAPDLVFNEYRMHKSRMYSQCVRMRHLSQEFGWLQITP 805
                                                                                                                                                 -PLAECKGSLLDDSAGKSTEDTAE----YSPFKGGYTKGLEGESLGCSGSAAAGSSGTLE 342
                                                                                                                                                                                                          343 LPSTLSLYKSGALDEAAAYQSRDYYNFPLALAGPPPPPPPPPPHARIKLENPLDYGSAWA 402
                                                                                                                                                                                                                                                                                                -ratpsrpge----aavtaapasasvssasssgstlecilykaegappqqgpfapppck 481
                                                                                                                                                                                                                                                                                                                                                          482 apgasgcllprdglpstsasaaaaga-apaly--palglng-----lpglgygaavlke 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCHYGALTCGSCKVFFKRAAEGKQKYLCASRNDCTIDKFRRKNCPSCRLRKCYEAGMTLG 631
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                                                      235 pllkgkpralggaa--agggaaacppgaaaggvalvpkedsrfsaprvalvegdapmapg
                                                                                         ------PPAVRPTPCA--
                                                                                                                                                                  GGGGGGGGGGGGGGGGGGGGGGGGAVAPYGYTRPPQGLACQESDFTAPDVWYPGGMVSR
                                                                                                                                                                                                                                                                                                                                                                                         -VPYPSPTCVKSEMGPWMDSYSGPYGDMRLETARDHVLPIDYYFP--PQKTCLICGDEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 APTSSKDNYLGGTSTISDNAKELCKAVSVSMGLG------VEALEHLSPG
                                                                                                                   293 rsplattvmdfihvpilplnhallaartrqlledesydggagaasafapp--rtspcass
                                                                                                                                                                                                                                                                    403 AAAAQCRYGDLASLHGAGAAGPGSGSPSAAASSSWH---TLFTAE-----EGQLYGPCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     866 LLDSVQPIARELHQFTFDLLIKSHMVSVDFPEMMAEIISVQVPKILSGKVKPIYFH 921
                                                                                                                                                                                                                             EQLRG----DCMYAPLLGV-----
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RESULT 15
AAY97297
ID AAY97297 standard; Protein; 933 AA.
XX
AC AAY97297;
XX
AC AAY97297;
XX
DT 03-JAN-2001 (first entry)
XX
BE Human progesterone receptor B-form.
XX
KW Recombinant DNA; gene therapy; hormone responsive element;
XX
KW Ransgene: HRE; haemophilia; clotting factor IX; vaccine;
XX
KW ransgene: HRE; haemophilia; clotting factor IX; vaccine;
XX
XX
OS Homo sapiens.
XX
XX
XX
XX

N W0200049147-A1. XX XX PD 24-AUG(2000.) 18-FEB-2000; 2000WO-EP01368. 19-FEB-1999; 99DE-1007099.

19-FEB-1999; 99US-0120848.
(THER-) THERAGENE BIOMEDICAL LAB GMBH.

Hauser-funke C;

WPI; 2000-549273/50.

N-PSDB; AAA53851

Novel nucleic acid construct useful in gene therapy comprising an hormone responsive element and transgene in which the hormone responsive element is not functionally linked to the transgene

Disclosure; Page 92-95; 100pp; English.

New nucleic acid constructs are described which comprise an hormone responsive element (HRE) and a transgene (T). Alternatively the nucleic acid construct, comprises at least one HRE and a transgene, where one of the HRRE is not functionally linked to the transgene, where one of the HRRE is not functionally linked to the transgene. The constructs preferably comprise a transgene which encodes a protein which is lacking in a variety of genetic disorders or involved in conditions related in inappropriate responses to hormones, for example hormone-dependent cancer. The transgene may also be used to replace a defective gene cancer. The transgene may also be used to replace a defective gene cancer. The transgene is human clotting factor IX can be used for resulting in such genetic disorders as haemophilia, von Millebrand disease, and cystic fibrosis. Vectors comprising these constructs where the transgene is human clotting factor IX can be used for treating blood clotting disorders such as haemophilia, von Millebrand disease, and cystic fibrosis. Vectors such as heamophilia when the transgene encodes a clotting factor IX. The administration to an organism or to a cellular system. The Constructs have applications in gene therapy for treating heamophilia when the davantage of this system is that the hormone receptor complex contains a hormone receptor that becomes activated after binding of its specific hormone receptor that becomes activated after binding of its specific normone responsive element. The presence of the hormone responsive element on the nucleic acid carrying a transgene encodes a link between the nucleic acid carrying the transgene and the hormone receptor complex. Thus the cell membrane.

Sequence 933 AA;

33; 68 dpsdektqdqqslsdvegaysraeatrgaggssssppekdsglldsvldtllapsgpgqs 127 125 LECHPERGCVPEPGAAVAASKG--LPQQLPAPPDEDDSAAPSTLSLLGPTFP-----GL 176 128 ------qpsppacevtsswclfgpelp----edppaapatgrvlsplmsrsgckvgd 174 ---QQQQQEAVSEGSSSGRAREASGA 219 67 QOQQQQQQQQQQQQQQCTSPRQQQQQGEDGSPQAHRRGPTGYL--VLDEEQQPSQPQSA 124 Gaps 8 gpraphvaggppspevgspllcrpaagpfpgsqtsdtlpevsaipisldgllfprpcqgq 67 99 ÖÖÖÖÖÖÖÖÖÖ 99 Indels 214; Length 933 Query Match 25.6%; Score 1256; DB 21; Best Local Similarity 34.5%; Pred. No. 2.5e-76; Matches 349; Conservative 119; Mismatches 329; -PGA-177 SSCSADLKDILSE--ASTMQLL--38 GPRHPEAASAAPq ōλ Qγ qq δ g Ω

263 293	319	357	407	431	459	518	537	576 580	636	640	069	700	750	160	810	820	870	880		
P-TSSKDNYLGGTSTISDNA	QLRGDCMYAPLLGVPPAVRPTPCAPLAECKGSLLDDSAGKSTEDTAEYSPFKGGYT				CRYGDLASLHGAGAAGPGSGSPSAAASSSWHTLFTAEEGQLYGPCGGGGGGGG			SPTCVKSEMGPWMDSYSGPYGDMRLETARDHVLPIDYYFPPQKTCLICGDEASGCHYG ::	ALTGGSCKVFFKRAAEGKQKYLCASRNDCTIDKFRRNCPSCRLRKCYEAGMTLGARRLK		KLGNLKLQEEGEASSTTSPTEETTQKLTVSHIEGYECQPIFLNVLEAIEPGVVC					.	MKALLLFSIIPVDGLKNQKFFDELRMNYIKELDRIIACKRKNPTSCSRRFYQLTKLLDSV		. QPIARELHQFTFDLLIKSHMVSVDFPEMMAEIISVQVPKILSGKVKPIYFH 921	
220	264	320	358	396	408	460	487	519	577	581	637	641	691	701	751	761	811	821	871	881
Qy Db	Qy	Qy	ογ	Dp	Qy Dp	δy	QΩ	Qy	Qy	Db	Qy	QQ	Qy	qq	Qy	QQ	ΟŊ	QQ	δÿ	qq

Search completed: January 3, 2002, 23:06:01 Job time: 5597 sec

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